

FIG. 1A

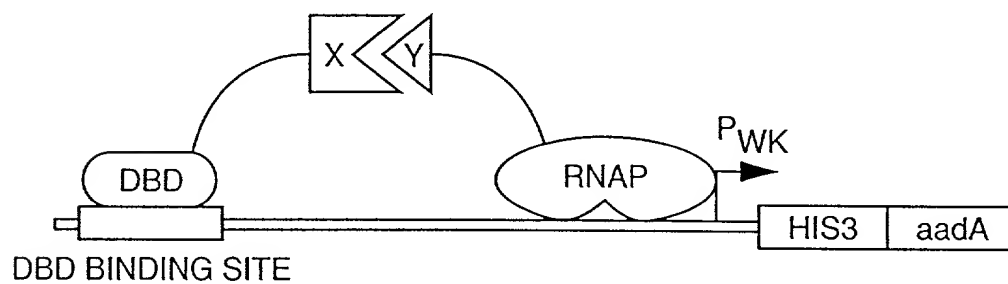


FIG. 1B

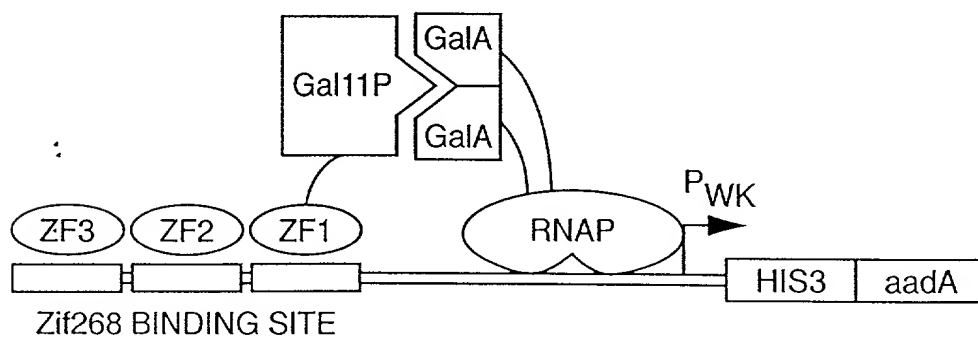


FIG. 1C

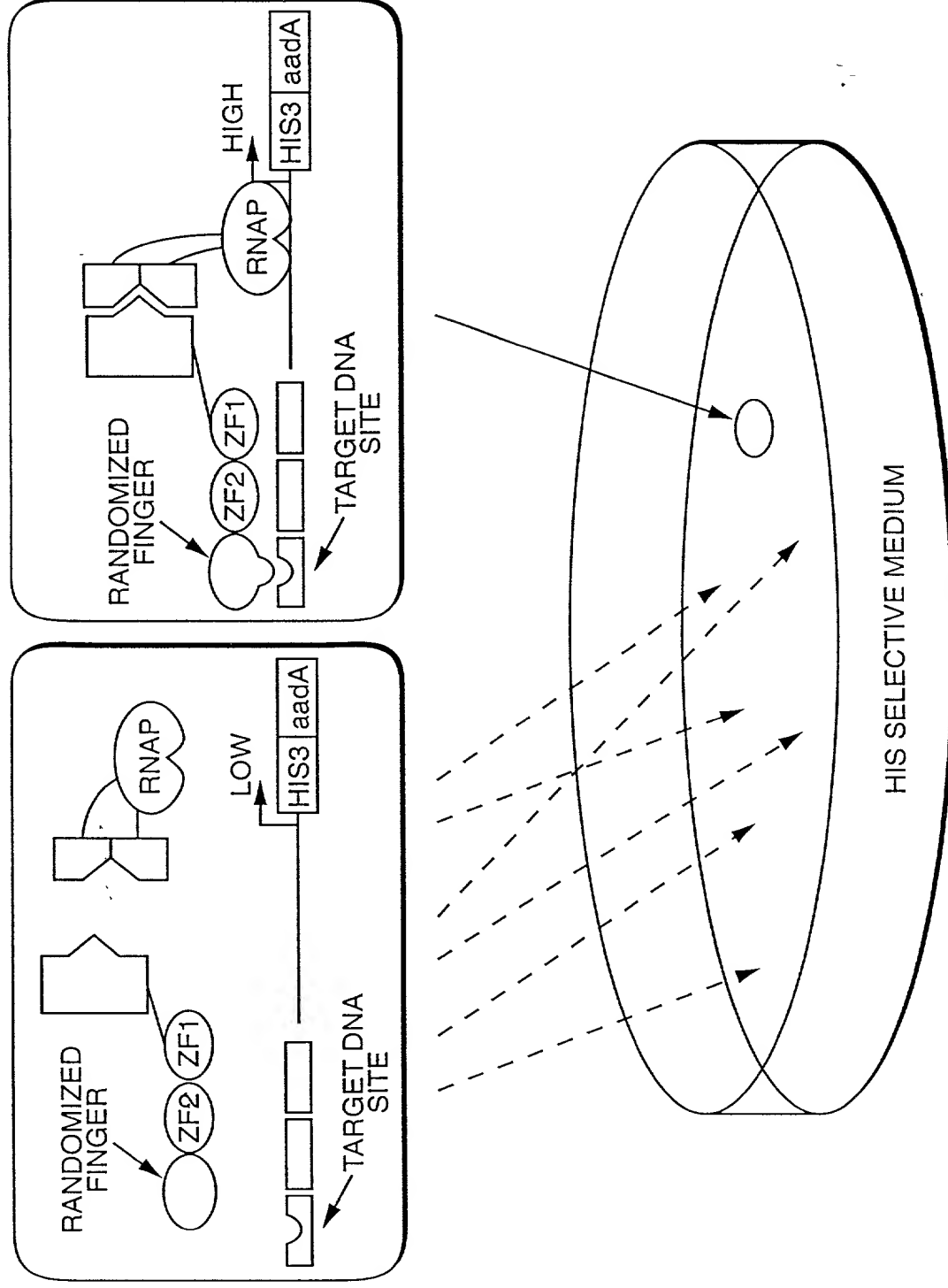


FIG. 2

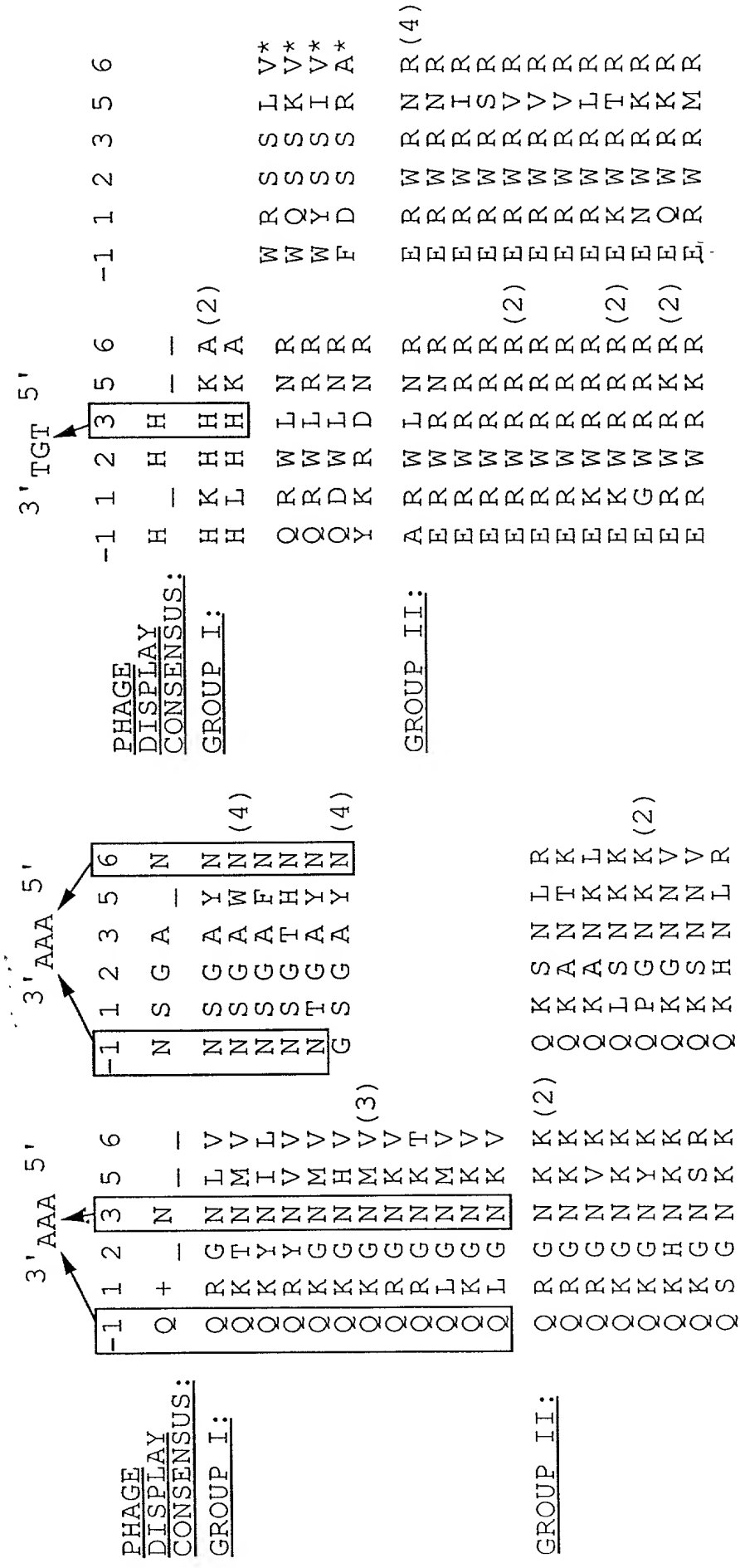


FIG. 3B

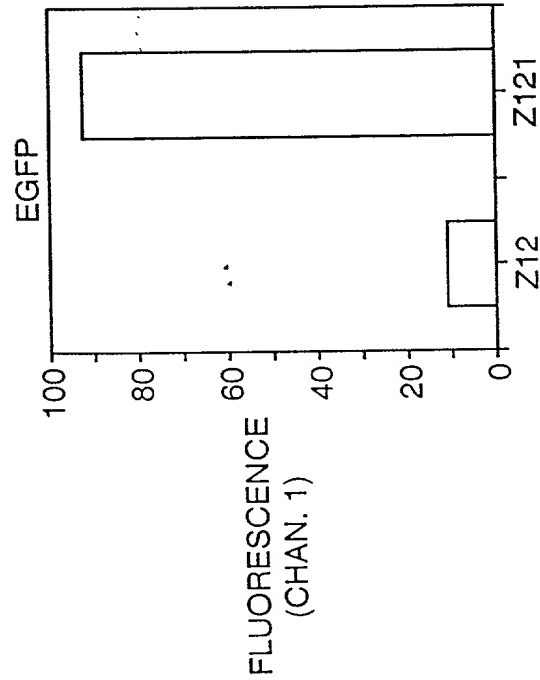


FIG. 4A

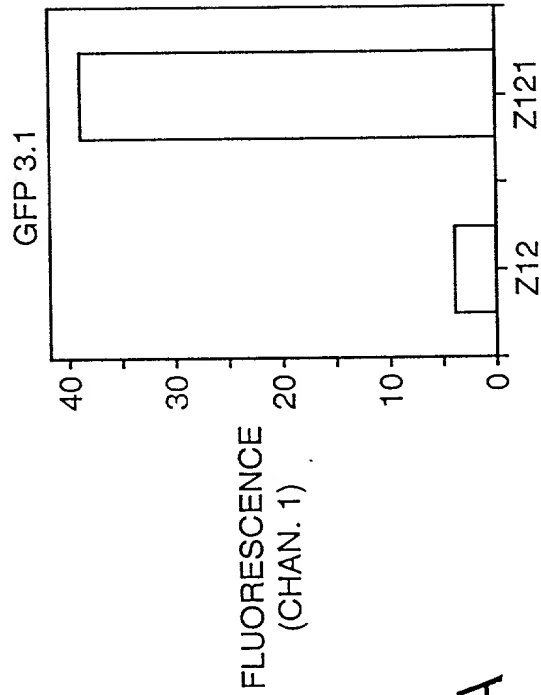


FIG. 4B

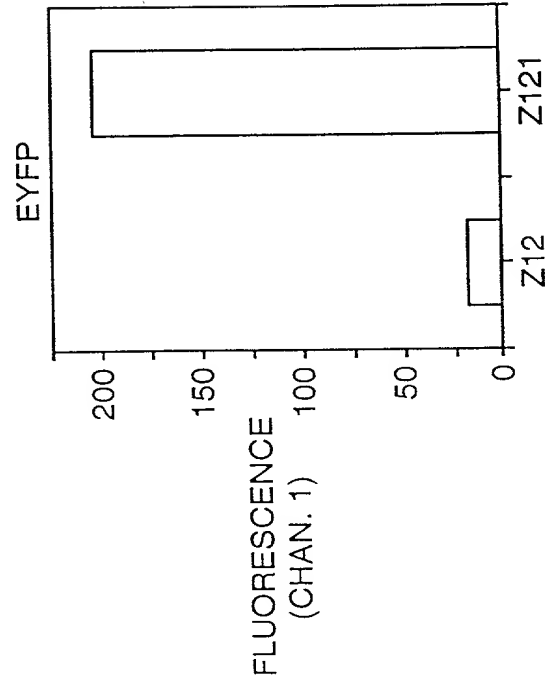


FIG. 4C

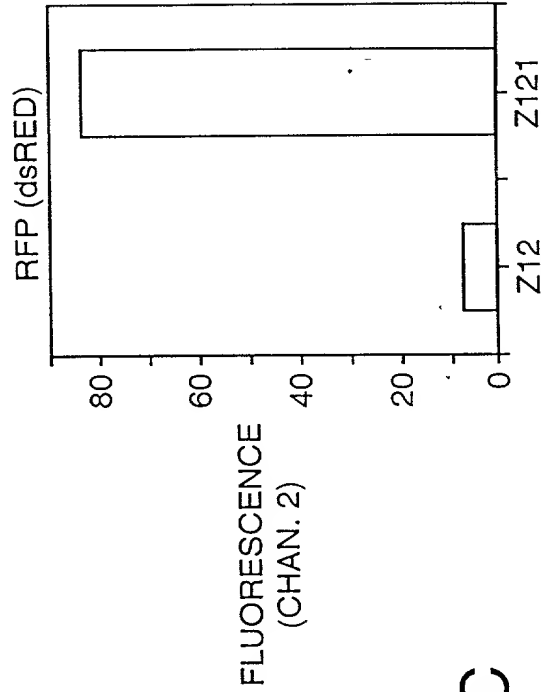


FIG. 4D

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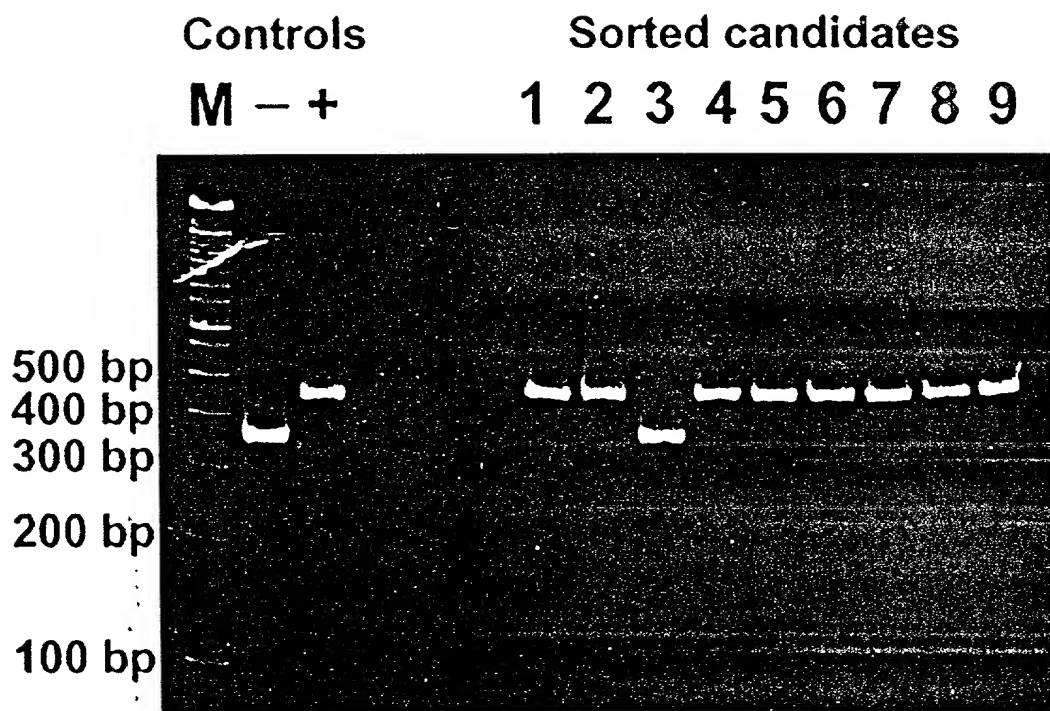


Fig. 5

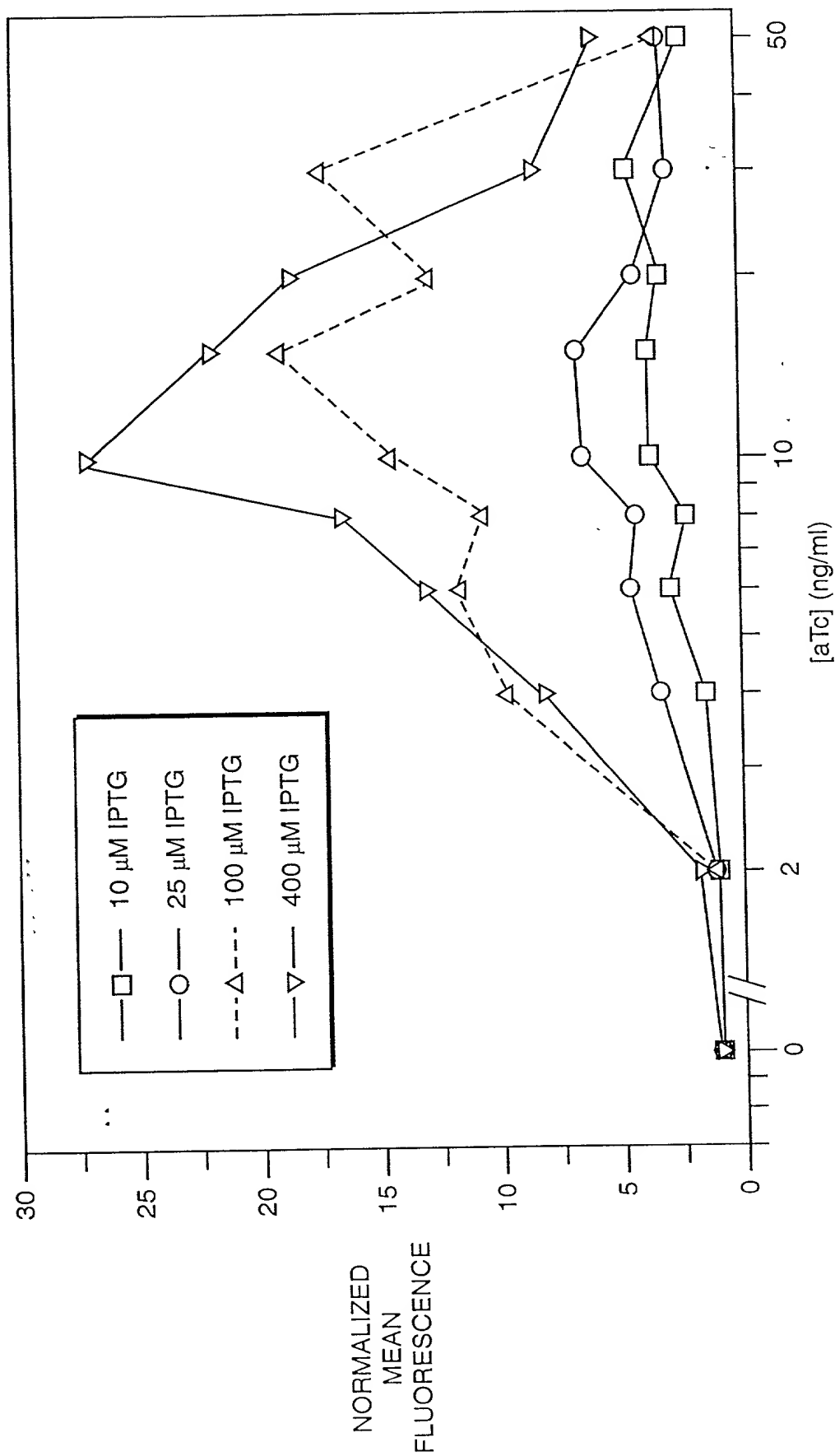


FIG. 6

REPORTER CONSTRUCT #2

REPORTER CONSTRUCT #1

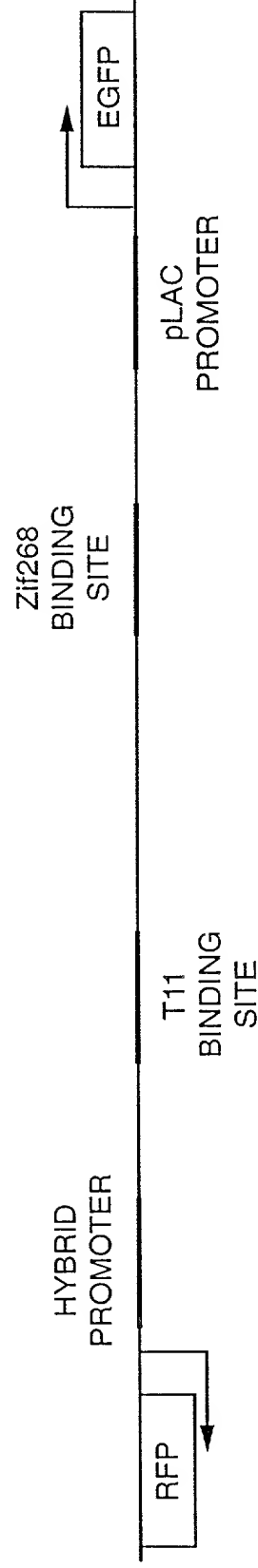


FIG. 7

FIG. 8A

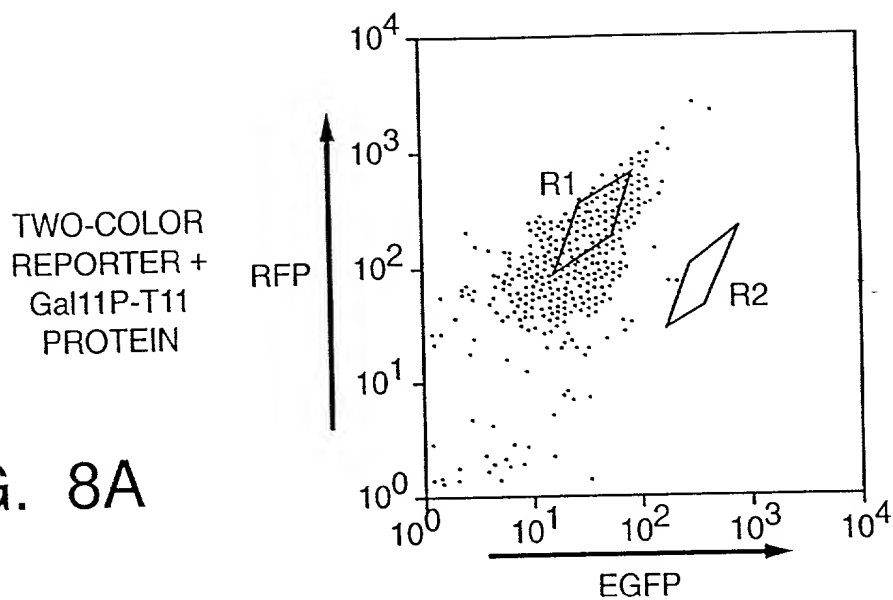


FIG. 8B

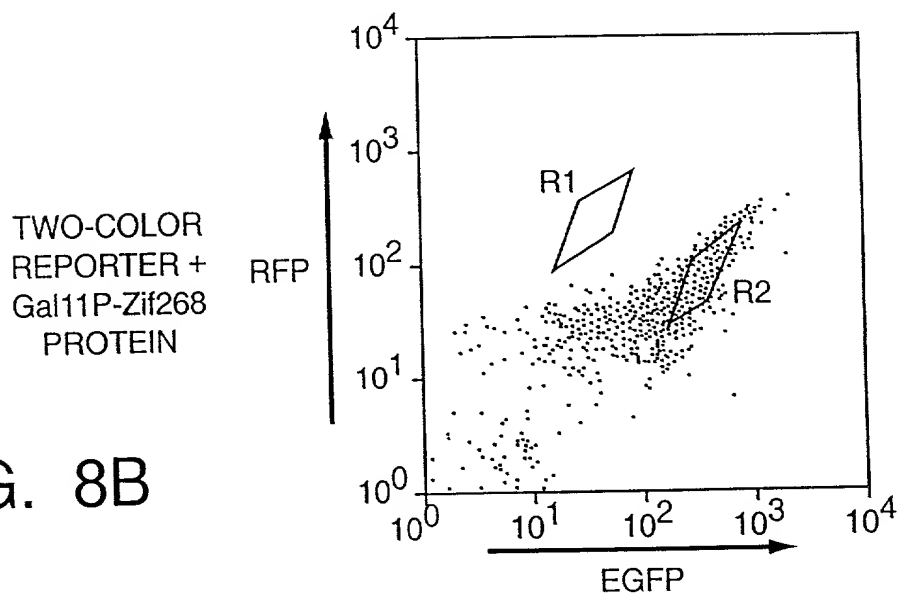
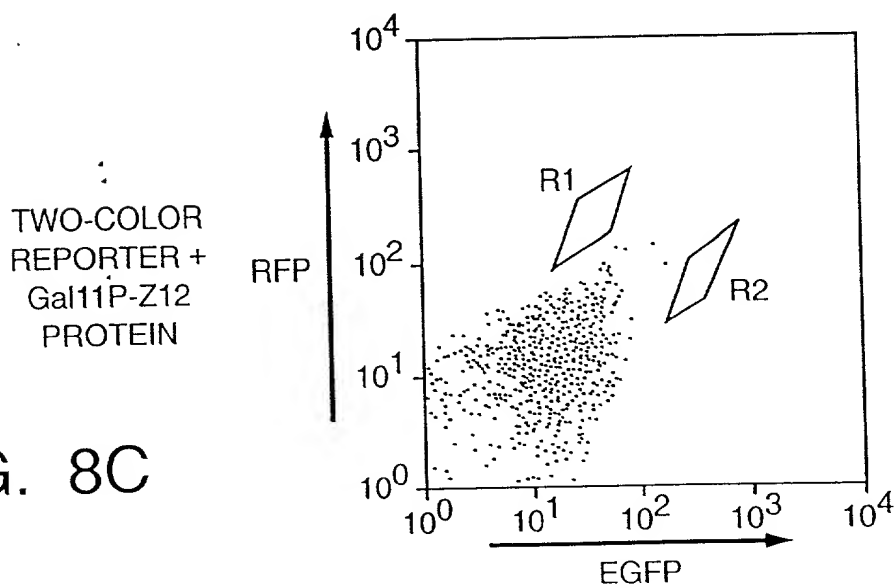


FIG. 8C



P53^{ZF} *IN VITRO* SITE SELECTION CONSENSUS SEQUENCE:

CXGGACACGTX

(WHERE X = NO CLEAR PREFERENCE)

IN VIVO SITE SELECTION LIBRARY

CGGGANNNNNG

(WHERE N = A MIXTURE OF A, G, C, AND T)

SELECTED CLONES:

SEQUENCE	# OF CLONES
CGGGACACGTG	9
CGGGACATGTG	5
CGGGACACGGG	2

SEQUENCE	FOLD ACTIVATION
CGGGACACGTG	18.6 ± 2.7
CGGGACATGTG	12.0 ± 0.5
CGGGACACGGG	12.6 ± 1.9

FIG. 9

FIG. 10

In vivo site selection

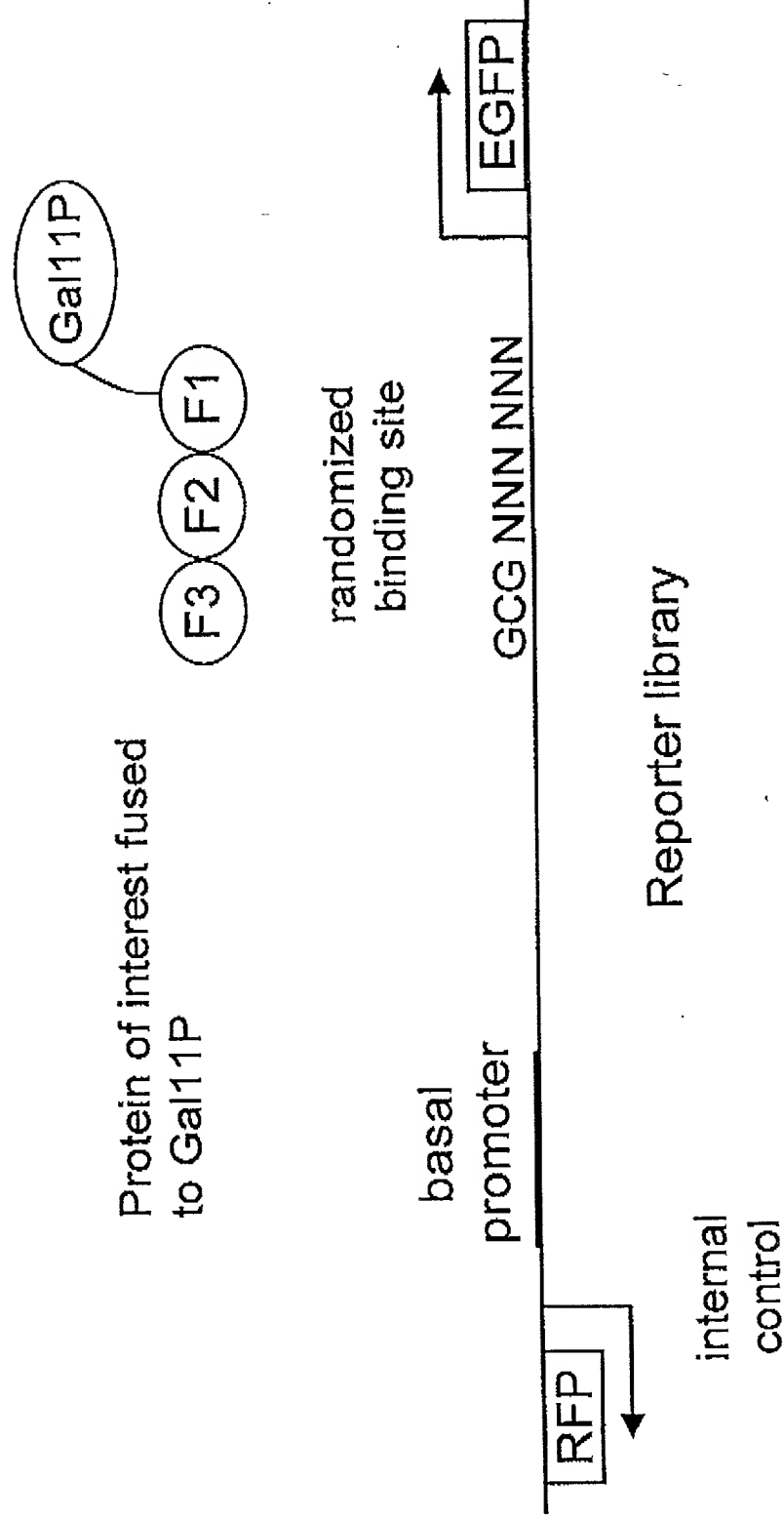


FIG. 11

Selecting Dimerization Domains

Tail to Tail

Variable spacing between sites

Randomized peptides on one monomer can interact with any portion of other monomer, only one possibility is shown

If using FACS version, can use half site driving RFP as counter-selection

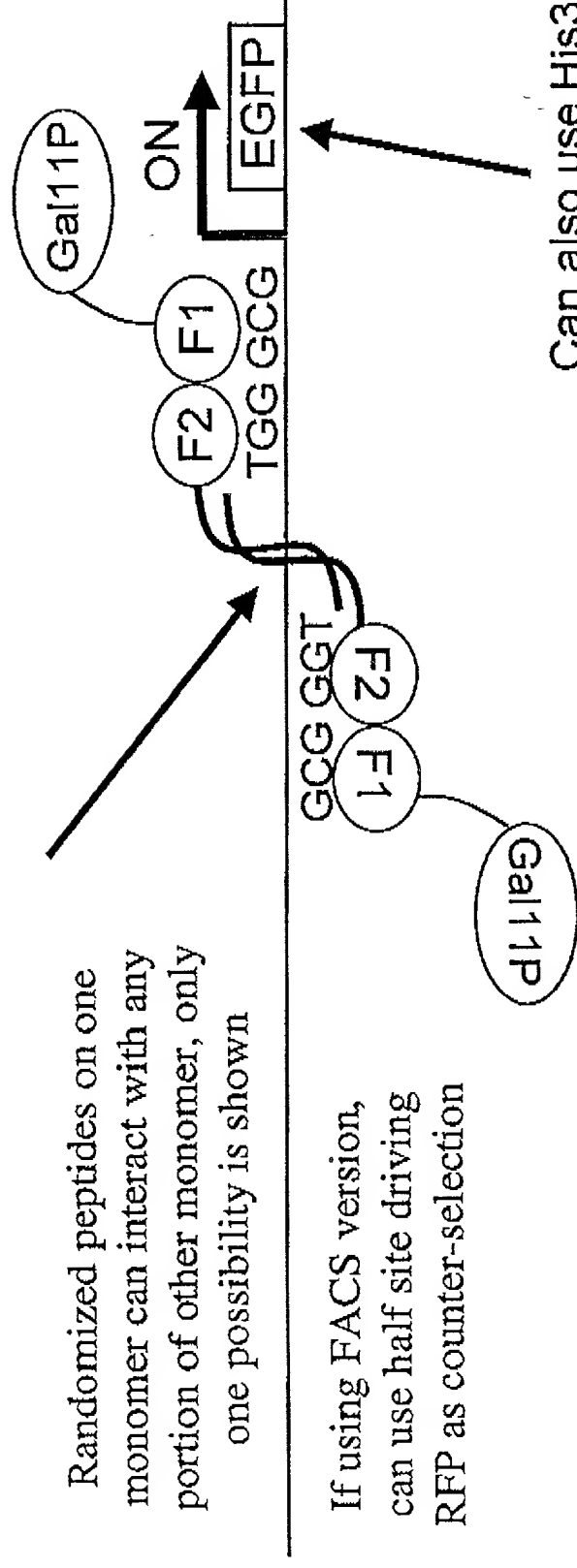
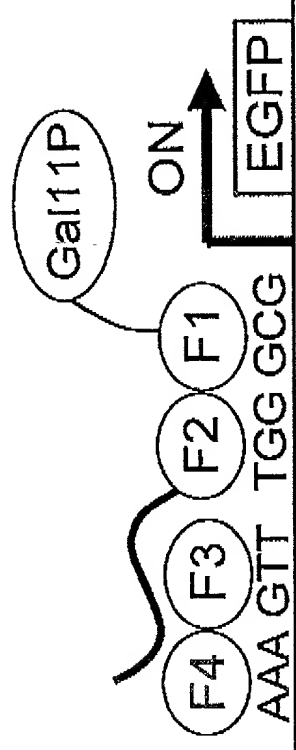


FIG. 12

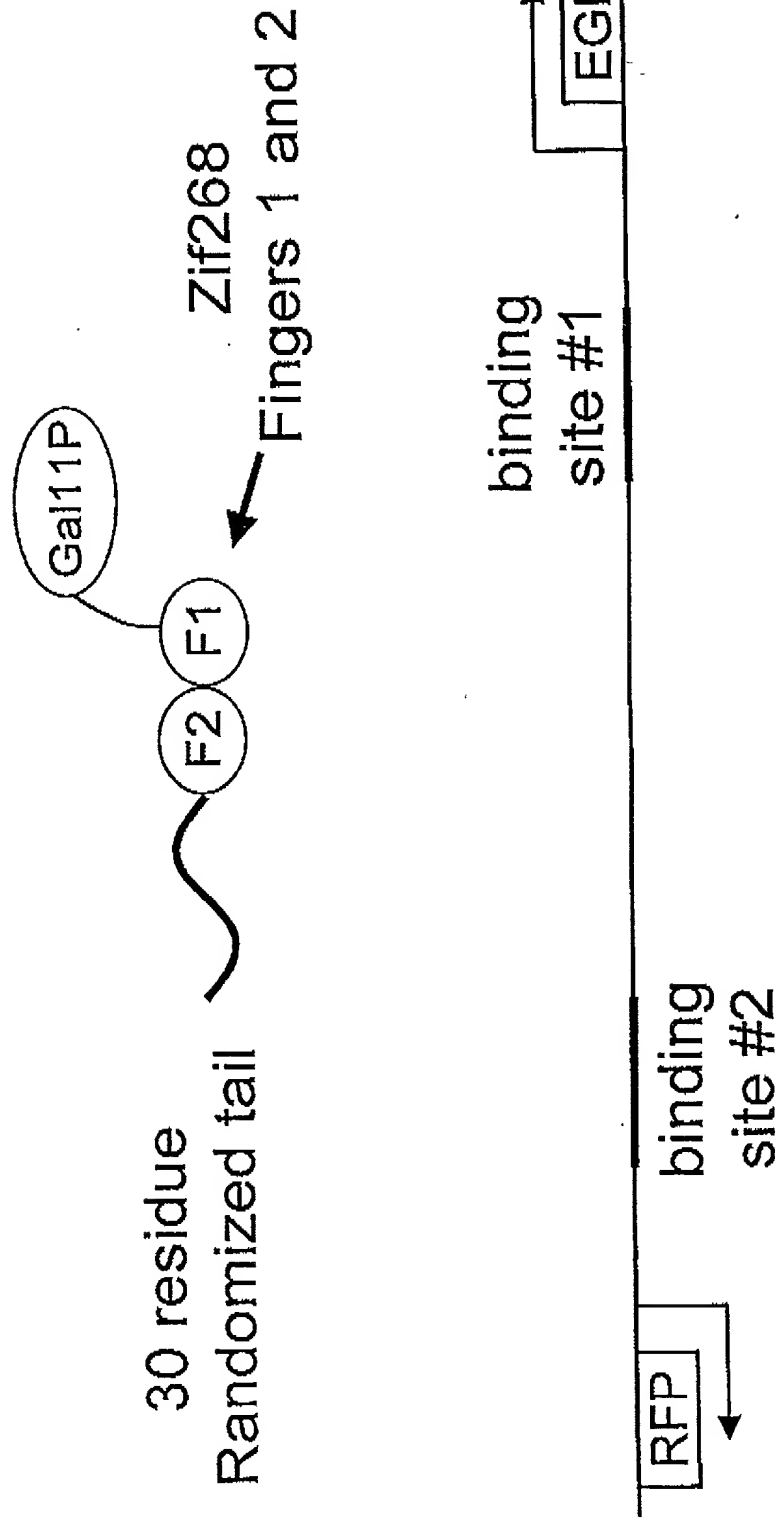
Selecting Dimerization Domains

Head to Tail

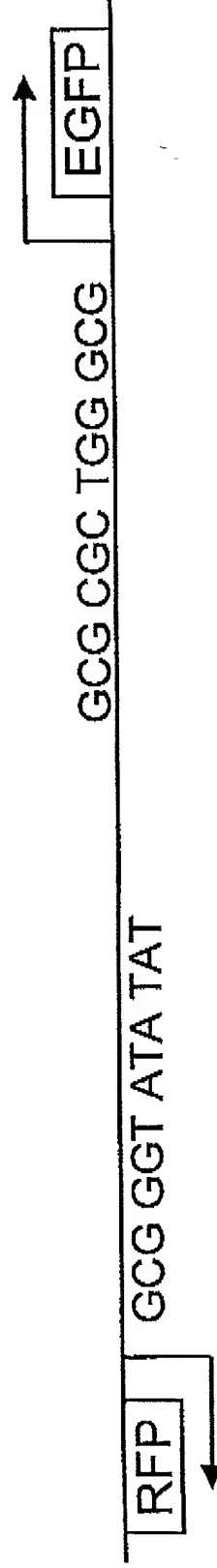
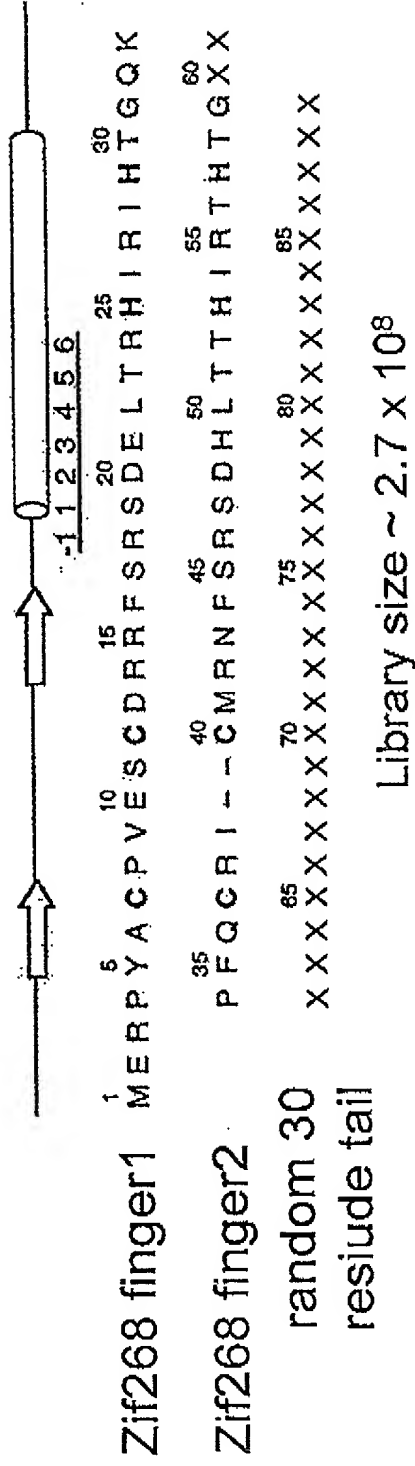


If using FACS version,
can use half site driving
RFP as counter-selection

Selecting sequence-specific domains from random peptides



Sequence of library and reporter



[illegible]

Sequence of library and reporter

